

SEQUENCE LISTING

<110> Hemmati-Brivanlou, Ali
Weinstein, Daniel C.

<120> TRANSLATION INITIATION FACTOR 4AIII, AND METHODS OF USE
THEREOF

<130> 600-1-211 N

<140> UNASSIGNED

<141> 1999-05-25

<160> 12

<170> PatentIn Ver. 2.0

<210> 1

<211> 1245

<212> DNA

<213> *Xenopus laevis*

<400> 1

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<210> 2

<211> 415

<212> PRT

<213> Xenopus laevis

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Thr Ser Glu Glu Val Asp Val Thr Pro Thr Phe Asp Thr Met Gly Leu
35 40 45

Arg Glu Asp Leu Leu Arg Gly Ile Tyr Ala Tyr Gly Phe Glu Lys Pro
50 55 60

Ser Ala Ile Gln Gln Lys Ala Ile Lys Gln Ile Ile Lys Gly Arg Asp
65 70 75 80

Val Ile Ala Gln Ser Gln Ser Gly Thr Gly Lys Thr Ala Thr Phe Cys
85 90 95

Val Ser Val Leu Gln Cys Leu Asp Ile Gln Ile Arg Glu Thr Gln Ala
100 105 110

Leu Ile Leu Ala Pro Thr Lys Glu Leu Ala Arg Gln Ile Gln Lys Val
115 120 125

Leu Leu Ala Leu Gly Asp Tyr Met Asn Val Gln Cys His Ala Cys Ile
130 135 140

Gly Gly Thr Asn Val Gly Glu Asp Ile Arg Lys Leu Asp Tyr Gly Gln
145 150 155 160

His Val Val Ala Gly Thr Pro Gly Arg Val Phe Asp Met Ile Arg Arg
165 170 175

Arg Ser Leu Arg Thr Arg Ala Ile Lys Met Leu Val Leu Asp Glu Ala
180 185 190

Asp Glu Met Leu Asn Lys Gly Phe Lys Glu Gln Ile Tyr Asp Val Tyr
195 200 205

Arg Tyr Leu Pro Pro Ala Thr Gln Val Cys Leu Ile Ser Ala Thr Leu
210 215 220

Pro His Glu Ile Leu Glu Met Thr Asn Lys Phe Met Thr Asp Pro Ile
225 230 235 240

Arg Ile Leu Val Lys Arg Asp Glu Leu Thr Leu Glu Gly Ile Lys Gln
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 Phe Phe Val Ala Val Glu Arg Glu Glu Trp Lys Phe Asp Thr Leu Cys
 260 265 270
 Asp Leu Tyr Asp Thr Leu Thr Ile Thr Gln Ala Val Ile Phe Cys Asn
 275 280 285
 Thr Lys Arg Lys Val Asp Trp Leu Thr Glu Lys Met Arg Glu Ala Asn
 290 295 300
 Phe Thr Val Ser Ser Met His Gly Asp Met Pro Gln Lys Glu Arg Glu
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 Ser Ile Met Lys Glu Phe Arg Ser Gly Ala Ser Arg Val Leu Ile Ser
 325 330 335
 Thr Asp Val Trp Ala Arg Gly Leu Asp Val Pro Gln Val Ser Leu Ile
 340 345 350
 Ile Asn Tyr Asp Leu Pro Asn Asn Arg Glu Leu Tyr Ile His Arg Ile
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 Gly Arg Ser Gly Arg Tyr Gly Arg Lys Gly Val Ala Ile Asn Phe Val
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 Lys Asn Asp Asp Ile Arg Ile Leu Arg Asp Ile Glu Gln Tyr Tyr Ser
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 405 410 415

<210> 3

<211> 532

<212> DNA

<213> Homo sapiens

<400> 3

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<210> 4

<211> 177

<212> PRT

<213> Homo sapiens

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Ile Gln Val Arg Glu Thr Gln Ala Leu Ile Leu Ala Pro Thr Arg Glu
35 40 45

Leu Ala Val Gln Ile Gln Lys Gly Leu Leu Ala Leu Gly Asp Tyr Met
50 55 60

Asn Val Gln Cys His Ala Cys Ile Gly Gly Thr Asn Val Gly Glu Asp
65 70 75 80

Ile Arg Lys Leu Asp Tyr Gly Gln His Val Val Ala Gly Thr Pro Gly
85 90 95

Arg Val Phe Asp Met Ile Arg Arg Arg Ser Leu Arg Thr Arg Ala Ile
100 105 110

Lys Met Leu Val Leu Asp Glu Ala Asp Glu Met Leu Asn Lys Gly Phe
115 120 125

Lys Glu Gln Ile Tyr Asp Val Tyr Arg Tyr Leu Pro Pro Ala Thr Gln
130 135 140

Val Val Leu Ile Ser Ala Thr Leu Pro His Glu Ile Leu Glu Met Thr
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Asn Lys Phe Met Thr Asp Pro Ile Arg Ile Leu Val Gly Ile Pro Ala
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<210> 5

<211> 1536

<212> DNA

<213> Homo sapiens

<400> 5

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gacccccacg ttcgacacca tgggcctgcg ggaggacctg ctgcggggca tctacgctta 240
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<210> 6

<211> 411

<212> PRT

<213> Homo sapiens

<400> 6

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Glu Val Asp Val Thr Pro Thr Phe Asp Thr Met Gly Leu Arg Glu Asp
35 40 45

Leu Leu Arg Gly Ile Tyr Ala Tyr Gly Phe Glu Lys Pro Ser Ala Ile
50 55 60

Gln Gln Arg Ala Ile Lys Gln Ile Ile Lys Gly Arg Asp Val Ile Ala
 65 70 75 80

Gln Ser Gln Ser Gly Thr Gly Lys Thr Ala Thr Phe Ser Ile Ser Val
 85 90 95

Leu Gln Cys Leu Asp Ile Gln Val Arg Glu Thr Gln Ala Leu Ile Leu
 100 105 110

Ala Pro Thr Arg Glu Leu Ala Val Gln Ile Gln Lys Gly Leu Leu Ala
 115 120 125

Leu Gly Asp Tyr Met Asn Val Gln Cys His Ala Cys Ile Gly Gly Thr
 130 135 140

Asn Val Gly Glu Asp Ile Arg Lys Leu Asp Tyr Gly Gln His Val Val
 145 150 155 160

Ala Gly Thr Pro Gly Arg Val Phe Asp Met Ile Arg Arg Arg Ser Leu
 165 170 175

Arg Thr Arg Ala Ile Lys Met Leu Val Leu Asp Glu Ala Asp Glu Met
 180 185 190

Leu Asn Lys Gly Phe Lys Glu Gln Ile Tyr Asp Val Tyr Arg Tyr Leu
 195 200 205

Pro Ser Ala Thr Gln Val Val Leu Ile Ser Ala Thr Leu Pro His Glu
 210 215 220

Ile Leu Glu Met Thr Asn Lys Phe Met Thr Asp Pro Ile Arg Ile Leu
 225 230 235 240

Val Lys Arg Asp Glu Leu Thr Leu Glu Gly Ile Lys Gln Phe Phe Val
 245 250 255

Ala Val Glu Arg Glu Glu Trp Lys Phe Asp Thr Leu Cys Asp Leu Tyr
 260 265 270

Asp Thr Leu Thr Ile Thr Gln Ala Val Ile Phe Cys Asn Thr Lys Arg
 275 280 285

Lys Val Asp Trp Leu Thr Glu Lys Met Arg Glu Ala Asn Phe Thr Val
 290 295 300

Ser Ser Met His Gly Asp Met Pro Gln Lys Glu Arg Glu Ser Ile Met
 305 310 315 320

Lys Glu Phe Arg Ser Gly Ala Ser Arg Val Leu Ile Ser Thr Asp Val
 325 330 335
 Trp Ala Arg Gly Leu Asp Val Pro Gln Val Ser Leu Ile Ile Asn Tyr
 340 345 350
 Asp Leu Pro Asn Asn Arg Glu Leu Tyr Ile His Arg Ile Gly Arg Ser
 355 360 365
 Gly Gln Tyr Gly Arg Lys Gly Val Ala Ile Asn Phe Val Lys Asn Asp
 370 375 380
 Asp Ile Arg Ile Leu Arg Asp Ile Glu Gln Tyr Tyr Ser Thr Gln Ile
 385 390 395 400
 Asp Glu Met Pro Met Asn Val Ala Asp Leu Ile
 405 410

<210> 7
 <211> 1682
 <212> DNA
 <213> Homo sapiens

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<210> 8

<211> 411

<212> PRT

<213> Homo sapiens

<400> 8

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Glu Val Asp Val Thr Pro Thr Phe Asp Thr Met Gly Leu Arg Glu Asp
 35 40 45

Leu Leu Arg Gly Ile Tyr Ala Tyr Gly Phe Glu Lys Pro Ser Ala Ile
 50 55 60

Gln Gln Arg Ala Ile Lys Gln Ile Ile Lys Gly Arg Asp Val Ile Ala
 65 70 75 80

Gln Ser Gln Ser Gly Thr Gly Lys Thr Ala Thr Phe Ser Ile Ser Val
 85 90 95

Leu Gln Cys Leu Asp Ile Gln Val Arg Glu Thr Gln Ala Leu Ile Leu
 100 105 110

Ala Pro Thr Arg Glu Leu Ala Val Gln Ile Gln Lys Gly Leu Leu Ala
 115 120 125

Leu Gly Asp Tyr Met Asn Val Gln Cys His Ala Cys Ile Gly Gly Thr
 130 135 140

Asn Val Gly Glu Asp Ile Arg Lys Leu Asp Tyr Gly Gln His Val Val
 145 150 155 160

Ala Gly Thr Pro Gly Arg Val Phe Asp Met Ile Arg Arg Arg Ser Leu
 165 170 175

Arg Thr Arg Ala Ile Lys Met Leu Val Leu Asp Glu Ala Asp Glu Met
 180 185 190

Leu Asn Lys Gly Phe Lys Glu Gln Ile Tyr Asp Val Tyr Arg Tyr Leu
 195 200 205

Pro Pro Ala Thr Gln Val Val Leu Ile Ser Ala Thr Leu Pro His Glu
 210 215 220

Ile Leu Glu Met Thr Asn Lys Phe Met Thr Asp Pro Ile Arg Ile Leu
 225 230 235 240

Val Lys Arg Asp Glu Leu Thr Leu Glu Gly Ile Lys Gln Phe Phe Val
 245 250 255

Ala Val Glu Arg Glu Glu Trp Lys Phe Asp Thr Leu Cys Asp Leu Tyr
 260 265 270

Asp Thr Leu Thr Ile Thr Gln Ala Val Ile Phe Cys Asn Thr Lys Arg
 275 280 285

Lys Val Asp Trp Leu Thr Glu Lys Met Arg Glu Ala Asn Phe Thr Val
 290 295 300

Ser Ser Met His Gly Asp Met Pro Gln Lys Glu Arg Glu Ser Ile Met
 305 310 315 320

Lys Glu Phe Arg Ser Gly Ala Ser Arg Val Leu Ile Ser Thr Asp Val
 325 330 335

Trp Ala Arg Gly Leu Asp Val Pro Gln Val Ser Leu Ile Ile Asn Tyr
 340 345 350

Asp Leu Pro Asn Asn Arg Glu Leu Tyr Ile His Arg Ile Gly Arg Ser
 355 360 365

Gly Arg Tyr Gly Arg Lys Gly Val Ala Ile Asn Phe Val Lys Asn Asp
 370 375 380

Asp Ile Arg Ile Leu Arg Asp Ile Glu Gln Tyr Tyr Ser Thr Gln Ile
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Asp Glu Met Pro Met Asn Val Ala Asp Leu Ile
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<210> 9

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:primer

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22

<210> 10

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:primer

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20

<210> 11

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:primer

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<210> 12

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:primer

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20